

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 2000, 14:05:47 ; Search time 18.88 Seconds
(without alignments) 776.469 Million cell updates/sec

Title: US-09-373-230-2

Sequence: 1 NFGRLCTAVLRINOVFL.....KKDNGKSVFTLTLNHS 157

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP:REMBL.14:.*
2: SP:archaea:.*
3: SP:bacteria:.*
4: SP:fungi:.*
5: SP:human:.*
6: SP:invertebrate:.*
7: SP:mammal:.*
8: SP:pmc:.*
9: SP:organelle:.*
10: SP:phase:.*
11: SP:plant:.*
12: SP:rodent:.*
13: SP:virus:.*
14: SP:vertebrate:.*
14: SP:unclassified:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	522	64.6	193	6	09UT73
2	91	11.3	987	5	09V718
3	85.5	10.6	784	5	09Y174
4	85.5	10.6	784	5	09U976
5	85	10.5	482	5	09U814
6	85	10.5	483	5	09Y046
7	83	10.3	267	13	073909
8	81	10.0	483	5	09Y677
9	80.5	10.0	267	6	029082
10	80.5	10.0	414	5	024892
11	80	9.9	506	2	084869
12	78.5	9.7	1039	1	09Y277
13	78	9.7	388	2	09RF17
14	78	9.7	1196	2	045916
15	78	9.7	1196	2	053550
16	78	9.7	1196	2	038197
17	78	9.7	1196	2	038197
18	78	9.7	1247	5	096168
19	77.5	9.6	366	12	09YWM0

20	77.5	9.6	1631	4	09Y606	09Y606 homo sapien
21	77	9.5	563	10	09SV96	09SV96 arabidopsis
22	77	9.5	672	5	09U0K1	09U0K1 plasmodium
23	76.5	9.5	905	3	094641	094641 schizosacch
24	76.5	9.5	1294	10	09S814	09S814 arabidopsis
25	76	9.4	525	4	09UF58	09UF58 homo sapien
26	75.5	9.3	161	11	062161	062161 mus musculu
27	75.5	9.3	626	2	050498	050498 streptomyc
28	75.5	9.3	818	10	09SN77	09SN77 arabidopsis
29	75.5	9.3	866	10	024295	024295 plismu sativ
30	75	9.3	621	2	09ZM42	09ZM42 helicobacte
31	75	9.3	1146	2	091778	091778 borrelia bu
32	74.5	9.2	661	2	073025	073025 synecocyst
33	74.5	9.2	803	4	075283	075283 homo sapien
34	74.5	9.2	849	11	09Z283	09Z283 homo sapien
35	74.5	9.2	950	4	09UN73	09UN73 borrelia bu
36	74.5	9.2	254	2	051029	051029 borrelia bu
37	74	9.2	445	5	09XVW4	09XVW4 dirosophila
38	73.5	9.1	647	3	002892	002892 saccharomyc
39	73.5	9.1	680	3	074343	074343 schizosacch
40	73.5	9.1	1128	10	09SAF6	09SAF6 arabidopsis
41	73.5	9.1	1146	2	068317	068317 vibrio chol
42	73.5	9.1	2077	12	09W733	09W733 human herpe
43	73.5	9.1	2077	12	09O337	09O337 human herpe
44	73	9.0	266	6	09TFK1	09TFK1 tursiops tr
45	73	9.0	1298	5	044199	044199 caenorhabdi

ALIGNMENTS

RESULT 1
ID 09UT73 PRELIMINARY; PRT: 193 AA.
AC 09UT73:
DT 01-MAY-2000 (TREMURel. 13, Created)
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)
DT 01-MAY-2000 (TREMURel. 13, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 20012648.
RA Shoda I.K., Zariwaga D.S., Hirano A., Brown W.C.;
RT Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity.*;
RL J. Interferon Cytokine Res. 19:1169-1177(1993).
DR EMBL: AF124789; AAF08686.1; -
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA9C4 CRC64;

Query Match 64.6%; Score 522; DB 6; Length 193;
Best Local Similarity 65.2%; Pred. No. 1.2e-40;
Matches 101; Conservative 30; Mismatches 22; Indels 2; Gaps 2;
OY 1 NFGRLCTAVLRINOVFLVDK-RQYFEDMTDIOASSEPOTRLIYWKSEVYGL 59
DB 37 HFCKLEPKRISILRNINDQVLFINGNQPVFEDMDPSQDNAPOTFLIYWKDILRGL 96
OY 60 AAVLSYKDSKXSTLSCNKRKIIISFEEDMPENDIDIOSDLFPQKRVPGH-NMEFESLY 118
DB 97 AAVLSYKDSKXSTLSCNKRKIIISFEEDMDPSQDNAPOTFLIYWKDILRGL 156
OY 119 EGFHLAGCKEDDAFLIKKDKNGKSVFTLTLNHS 153
DB 157 KGFLACKKENDFLIKKDKNGKSVFTLTLNHS 191
RESULT 2
09V718

ID	09YJ14	PRELIMINARY:	PR:	784 AA.
AC	09YJ14:			
AD	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)		
DE	RETINOID X RECEPTOR RXR-2.			
OS	Schistosoma mansoni (Blood fluke).			
OC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida.			
OC	Schistosomatidae; Schistosomatidae; Schistosoma.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-NMRI:			
RX	MEDLINE; 99307140.			
RA	Friedern W.J., Niles E.G., Loverde P.T.;			
RT	"RXR-2, a member of the retinoid x receptor family in Schistosoma mansoni."			
RL	Gene 233:33-38(1999).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
DR	EMBL; AF129816; AAD33428.1; -.			
DR	INTERPRO; IPR000324; -.			
DR	INTERPRO; IPR000536; -.			
DR	INTERPRO; IPR01628; -.			
PFAM; PF00104; hormone_rec. 1.				
PFAM; PF00105; zf-C4; 1.				
DR	PRINTS; PRO0047; STROIDEFINGER.			
DR	PRINTS; PRO0350; VITAMINDR.			
DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.			
KW	Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger			
SO	SEQUENCE			
	784 AA; 87249 MW; CD35E449E5FD547F CRC64;			

Query Match	10.6%:	Score 85.5:	DB 5:	Length 784:
Best Local Similarity	27.1%:	Pred. No. 6.6:		
Matches 32:	Conservative 18:	Mismatches 53:	Indels 15:	Gaps
QY	46	LIITYMKDSEVRLAVLTLSVKDSKXSTLSCKNKRIISFEEMDPDEN-IDDIQSDLIF----	100%	
DBj	513	LVYMIADMLKPRISSTNSKTLPTPTINSTIDPENSISDKSCCTIQMK	5722	
QY	101	FORVPEGHNMKE-FESSLYEGHFLPACCKEDDAFRLLIKKDDGKDXSWMTTLNLHOS	157	
DBj	573	INKSVPLDEKMDYYISNPFEPHLL-----NNLTKPMDDNNNDISSKPTNINDN	621	
RESULT	4			
Q09096		PRELIMINARY;	PRT;	784 AA.
AC	Q09096;			
DT	01-MAY-2000 (TremBLrel. 13, Created)			
DT	01-MAY-2000 (TremBLrel. 13, Last sequence update)			
DT	01-JUN-2000 (TremBLrel. 14, Last annotation update)			
DE	REFID= X-RECEPTOR.			
GN	RXR.			
OS	Schistosoma mansoni (Blood fluke).			
OC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;			
CC	Schistosomatidae; Schistosomatidae; Schistosoma.			
RA	[1]			
RA	SEQUENCE FROM N.A.			
RA	Mendoza R.L., Escrivá H., Bouton D., Vanacker J.-M., Zelus D.,			
RA	Bonnelye E., Pierce R., Laudet V.;			
RT	"A Schistosoma mansoni nuclear receptor of the RXR family shows marked			
RT	structural and functional divergence from vertebrate and arthropod			
RT	homologs."			
RL	Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.			
EMBL:	AF158102; AAD45325.1; -.			
DR	INTERPRO: IPR000324; -.			
DR	INTERPRO: IPR000536; -.			
DR	INTERPRO: IPR001628; -.			
DR	INTERPRO: IPR001723; -.			
DR	PFAM: PF00104; hormone_rec; 1.			
DR	PFAM: PF00105; zf-C4; 1.			
DR	PRINTS: PR00047; STROIDINGER.			

Sat Nov 25 20:13:01 2000

us-09-373-230-2.rspt

Page 3

DR PRINTS: PRO0350; VITAMINDR.
DR PRINTS: PRO0398; STRDHOMONER.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR. 1.
KW Receptor.
SQ SEQUENCE 784 AA; 87250 MW; 471DAE9EB135A9F CRC64;

Query Match 10.6%; Score 85.5; DB 5; Length 784;
Best Local Similarity 27.1%; Pred. No. 6.6;
Matches 32; Conservative 18; Mismatches 53; Indels 15; Gaps 4;
OY 46 LIYWKDESEVGLAVTISVDSKXSTLSCKKTISEEMPPEN-IDDIQSOLF----- 100
DB 513 LVYWLANDHPRSLSTSTNSKSLPDTPTTINSDISNTITDDPEKSIDSKCTIOAK 572
OY 101 FOKRVPGNHME-FESSLYEGHFLACOKEDDAFKLKKKDNDSKVSMTLNLHOS 157
DB 573 INKSVPLDERKMDYYSNPEPHLL-----NNLIRPMDNNNDISSKPTINNDN 621

RESULT 5
OY0A14 PRELIMINARY; PRT: 482 AA.
AC OY0A14;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE PROTEIN PHOSPHATASE 2A 55 KDA REGULATORY B SUBUNIT (FRAGMENT).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyostelida; Dictyostellium.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99379588.
RA Murphy M.B., Levi S.K., Egelhoff T.T.;
RT "Molecular characterization and immunolocalization of Dictyostelium
RT discoideum protein phosphatase 2A.";
RL FEBS Lett. 456:7-12(1999).
DR EMBL; AF138279; AAD29694.1; -.
DR INTERPRO; IPR000009; -.
DR INTERPRO; IPR001680; -.
DR PFAM; PF01240; PR55_1.
DR PRINTS; PRO0600; PP2APR55.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
DR PROSITE; PS01024; PR55_1; 1.
DR PROSITE; PS01025; PR55_2; 1.
FT NO_TER 1
SQ SEQUENCE 482 AA; 55107 MW; 95E879E7A37D2392 CRC64;

Query Match 10.5%; Score 85; DB 5; Length 482;
Best Local Similarity 25.9%; Pred. No. 4.2;
Matches 36; Conservative 23; Mismatches 58; Indels 22; Gaps 6;
OY 14 NINDQVL-FYDKRQVFEEDMDIDIOSASEQTRLIYWKDESEVGLAVTISVDSKXST 72
DB 236 NINTECFNVVDIKPTNMDLELVITSAEHPPTSCNIFMYSSK-----GTLKGLDRSSA 290
OY 73 LSCNKKITSEEMDPENIDDIQSOLFPOKRVGNHMEFESSLYEGHFLACOKEDDAF 132
DB 291 L-CDNHAKVPEEEDPSNKS-----FSEIITISIDIKFSR---DQRYILSD----- 334
OY 133 KLILKKKDNDSKVSMTL 151
DB 335 FLTLKMDINMENKPKYKTI 353

RESULT 6
OY0A6 PRELIMINARY; PRT: 483 AA.
AC OY0A6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE PROTEIN PHOSPHATASE 2A B55 REGULATORY SUBUNIT.
GN PPP.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyostelida; Dictyostellium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AX4.
RA Campanha R.B., Etcheberry L.C., da Silva A.M.;
RT "Functional analysis of a B regulatory subunit of protein phosphatase
RT 2A in D. discoideum.";
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF167979; AAD45396.1; -.
DR INTERPRO; IPR000009; -.
DR INTERPRO; IPR001680; -.
DR PFAM; PF01240; PR55_1.
DR PRINTS; PRO0600; PP2APR55.
DR PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
DR PROSITE; PS01024; PR55_1; 1.
DR PROSITE; PS01025; PR55_2; 1.
SQ SEQUENCE 483 AA; 55275 MW; DCF9434FE95C7BE CRC64;

Query Match 10.5%; Score 85; DB 5; Length 483;
Best Local Similarity 25.9%; Pred. No. 4.2;
Matches 36; Conservative 23; Mismatches 58; Indels 22; Gaps 6;
OY 14 NINDQVL-FYDKRQVFEEDMDIDIOSASEQTRLIYWKDESEVGLAVTISVDSKXST 72
DB 237 NINTECFNVVDIKPTNMDLELVITSAEHPPTSCNIFMYSSK-----GTLKGLDRSSA 291
OY 73 LSCNKKITSEEMDPENIDDIQSOLFPOKRVGNHMEFESSLYEGHFLACOKEDDAF 132
DB 292 L-CDNHAKVPEEEDPSNKS-----FSEIITISIDIKFSR---DQRYILSD----- 335
OY 133 KLILKKKDNDSKVSMTL 151
DB 336 FLTLKMDINMENKPKYKTI 354

RESULT 7
OY03909 PRELIMINARY; PRT: 267 AA.
AC OY03909;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE INTERLEUKIN-1BETA.
GN IL-1BETA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RA Weinig K.C., Sick C., Kaspers B., Staeheli P.;
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; Y15006; CAA75239.1; -.
DR HSSP; P18510; 1IRA.
DR INTERPRO; IPR000975; -.
DR PFAM; PF00340; Interleukin-1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
FT CHAIN 106 267 INTERLEUKIN-1BETA.
SQ SEQUENCE 267 AA; 29822 MW; 3BF72164EAD0B64 CRC64;

Query Match 10.3%; Score 83; DB 13; Length 267;
Best Local Similarity 24.8%; Pred. No. 3.2;
Matches 30; Conservative 18; Mismatches 45; Indels 28; Gaps 4;
OY 31 DMTDIDIOS-----ASEQTRLIYWKDESEVGLA-----VTLISYK 66
DB 118 DIFDINQKCFVLESPQVALHLOQPSOSSOKRVNLIALYRPRGSGAGTQMPVALGK 177

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OY      67 DSK-----XSTJSCNKKNIISFEEMDPPEPIDIO-SDJLFPCKRVGNKMKKESSIEVGEHF 122
          :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      178 GYLWYSCHWSMGTEPIPLQLEADVDKIDBSVELTRFTFRKLDSPTSEGTTFEESAAPGWF 237

OY      123 L 123
          :
DB      238 I 238

RESULT   8
O9XV67    PRELIMINARY; PRT; 483 AA.
AC O9XV67;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
GN F25C8.2 PROTEIN.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdittida; Rhabditoidea;
RN Rhabdittidae; Peloderinae; Caenorhabditis.
[1]
RX SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA Matthews L.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL elegans.";
RT Submitted (NOV-1996) to the EMBL/genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kerhaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkseen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thelery-Mieg Y., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A.J., Weinstock L., Wilkinson-Spoat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL, Z81512; CAB04171.1; -.
DR INTERPRO: IPRO02937; -.
SR PFAM; PF01593; Amino_oxidase; 1.
SQ SEQUENCE 483 AA; 55505 MW; 172CEC9149557AB CRC64;

Query Match 10.0%; Score 81; DB 5; Length 483;
Best Local Similarity 26.4%; Pred. NO. 9.8;
Matches 55; Conservative 24; Mismatches 63; Indels 66; Gaps 12,

OY      3 GRHCTTAATIRMINOV-----LFVDKRQPVFEDMTDIOQSAS-----EPQTRLII 48
          |||:::||||||::||::||::||::||::||::||::||::||::||::||::||::||
DB      81 GLYHGGAETVNGVDDEVYNLVKEKYDF-DKTRPRDDIMMDLDODNSTLYVNGHLVPKTL 139

OY      49 YMYKDSEVAGLAVLTSVKSKSXSTLCKKKIIS-FEEM--DPDENIDDIQSOLFQKRV 105
          ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      140 DKFND-YIRYLNVALYENKSIKINQLSVENEINNOGLEIFLRDVDPENDHEYESLINYK-- 196

OY      106 PGHNKMEPESLIYEGHFL-----ACQKEDDA-----FKILK 137
          |::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      197 ---NYFGQEMSSPYGELSLSNLSINDGDTEEDSDVLVKNQGYYELLKPKRSKIIPAGNIRL 253

OY      138 -----KKDENGDKSVAFETLTN---LH 155
          ::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      254 NCEVINVKREEN----INVTLTKNGEVLLH 277

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ID	Q29082;	PRELIMINARY;	PRT;	267 AA.
AC	Q29082;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DR	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)			
DE	INTERLEUKIN 1-BETA.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Vanderbroeck K.;			
RC	TISSUE=LIVER;			
RL	Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Van Damme J., Opendakker G., Billiau A.;			
RT	"Gene sequence, cDNA construction, expression in Escherichia coli and genetically approached purification of porcine interleukin-1 beta.";			
RL	Eur. J. Biochem. 217:45-52(1993).			
DR	EMBL; X74568; CAA52660.1; -.			
DR	HSSP; P01584; 1HTB.			
DR	INTERPRO; IPR000975; -.			
DR	INTERPRO; IPR002348; -.			
DR	PFAM; PF00340; Interleukin-1; 1.			
DR	PRINTS; PR00262; IL1HBGf.			
DR	PRINTS; PR00264; INTERLEUKIN1.			
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.			
SO	SEQUENCE 267 AA; 29893 MW; 4830645DA5FF9967 CRC64;			
Query Match	10.0%;	Score 80.5;	DB 6;	Length 267;
Best Local Similarity	28.6%;	Pred. No. 5.5;		
Matches 24;	Conservative 22;	Mismatches 25;	Indels 13;	Gaps 6;
QY	53 DSEVGGLAVTISVKRSKXSTLSCKNK---IISFEEMP---PENIDDIQSLLPIFFQRKV 105			
DB	165 DSDDK-IPTTLTGIK-GKNLYISCVMKKDPTPLQLLEDVDPKSPKR--DMERKFVFYKTEI 220			
QY	106 PGHNMEFESSLYEGHFLAACOKED 129			
DB	221 --KNRVEFSALYPMWYSTSQAE 242			
RESULT 10				
Q24892				
ID	Q24892	PRELIMINARY;	PRT;	414 AA.
AC	Q24892;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-JUN-2000 (TREMBLrel. 14, last annotation update)			
DE	CALMODULIN-DOMAIN PROTEIN KINASE (FRAGMENT).			
OS	Elmeria maxima.			
OC	Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Elmeriidae;			
OC	Elmeria.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-HOUGHTON;			
RA	MEDLINE; 96089387.			
RA	Bumstead J.M., Dunn P.P.J., Tomley F.M.;			
RT	"Nitrocellulose immunoblotting for identification and molecular gene			
RT	cloning of Elmeria maxima antigens that stimulate lymphocyte			
RT	proliferation."			
RL	Clin. Diagn. Lab. Immunol. 2:524-530(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-HOUGHTON;			
RA	MEDLINE; 97048698.			
RA	Dunn P.P.J., Bumstead J.M., Tomley F.M.;			
RT	"Sequence, expression and localization of calmodulin-domain protein			

kinases in *Eimeria tenella* and *Eimeria maxima*.";
 RL Parasitology 113:439-448(1996).
 DR EMBL: Z71756; CAA96438.1; -.
 DR HSSP: O63450; 1A06.
 DR INTERPRO: IPR000719; -.
 DR INTERPRO: IPR002048; -.
 DR INTERPRO: IPR002290; -.
 DR PFAM: PF00036; ehand; 4.
 DR PFAM: PF00069; kinase; 1.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN; 4.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR NON_TER 1
 FT SEQUENCE 414 AA; 47427 MW; 7B0C793F0A45BA68 CRC64;

Query Match 10.0%; Score 80.5; DB 5; Length 414;
 Best Local Similarity 25.7%; Pred. No. 9.1;
 Matches 29; Conservative 21; Mismatches 42; Indels 21; Gaps 4;

QY 42 PQRLLIYWNDEVRGLA-----VLSVDS-----KXSTLSCNNKLIISFEEMDPENI 91
 DB 174 PWRKVSPPAKDLIRKMLAYVPSMRISADALDHPWIKSTDTAKDSI-----NL 223
 QY 92 DDIOSDLFFQKRVPGHNMKEFESSLYEGHFLACOKEDDAFKLKKRKGENDG 144
 DB 224 PLSLESTILNI-ROFGTOKLAAMAAALYMGSKLTNEETDELNKIFQMKRNGD 275

RESULT 11
 ID 084869 PRELIMINARY; PRT; 506 AA.
 AC 084869;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
 DE HYPOTHEICAL 56.5 KDA PROTEIN.
 GN CT861.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D/W-3/CX;
 RX MEDLINE: 99000809.
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis.";
 RL Science 282:754-759(1998).
 DR EMBL: AE001359; AAC68459.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 506 AA; 56464 MW; 4FAAA12C1098B4 CRC64;

Query Match 9.9%; Score 80; DB 2; Length 506;
 Best Local Similarity 25.0%; Pred. No. 13;
 Matches 38; Conservative 25; Mismatches 55; Indels 34; Gaps 7;

QY 1 NFGRLCTAVIRNINDQVLFVKRQPVFEDMTDIDOSASPPQRLIYWNDEVRGLA 60
 DB 63 SFSRLQPTTP-----KERILFFGS-SPSSQLSSYTRTTSSPMW-----LFSNSQTRNST 111
 QY 61 VTLVSDSKXSTLSCNN-KLISFEEMDPENIDIOSDLFFQKRVPGHNMKEFESSLY 118
 DB 112 RLKSLKLFSSLSARSTSPSSSEPIKPSNL-----LHPEHHK-ELFSSIK 159
 QY 119 EGHFLACOKEDDAF-----KLKKRKE 141
 DB 160 KDNLSPIMEIDSPSATESLERLVTOKKE 191

RESULT 12

Q9YF27
 ID Q9YF27 PRELIMINARY; PRT; 1039 AA.
 AC Q9YF27;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
 DE HYPOTHEICAL 120.0 KDA PROTEIN APE0413.
 GN APE0413.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Desulfurococcaceae; Desulfurococcaceae;
 OC Aeropyrum.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K1;
 RX MEDLINE: 99310339.
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S., Anai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushiida N., Oguchi A., Aoki K., Kubota K., Nakamura Y.,
 RA Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT Crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 DR EMBL: AP000059; BAA79369.1; -.
 DR INTERPRO: IPR000330; -.
 DR INTERPRO: IPR001410; -.
 DR INTERPRO: IPR001650; -.
 DR PFAM: PF00176; SNE2_N; 1.
 DR PFAM: PF00271; helicase_C; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1039 AA; 119959 MW; 30C919184575F9D CRC64;

Query Match 9.7%; Score 78.5; DB 1; Length 1039;
 Best Local Similarity 26.4%; Pred. No. 40;
 Matches 37; Conservative 14; Mismatches 50; Indels 39; Gaps 5;

QY 31 DMTDIDOSASPPQRLIYWNDEVRGLA-----YKDSVNGLAFLVSDSKXSTL 73
 DB 374 DGEIDDEIDEEFERLAIFYFDKLLDPMFREELKKAQYAEIDILGKAV-----DSKVETL 428
 QY 74 SCNNKLIISFEEMDPENIDIOSDLFFQKRVPGHNMKEFESSLYEGHFLACOKEDDAFK 133
 DB 429 ---KRLGLVLTTPPEELDPBFKDLA-SOKAIVTFEFKDTATLYE-----K 471
 QY 134 LIKKRKGENDSKSVFTLTN 153
 DB 472 LRKMADEDFGDPGIVRFTS 491

RESULT 13
 ID Q9YF17 PRELIMINARY; PRT; 388 AA.
 AC Q9YF17;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
 DE PROTEIN I/II V-REGION (FRAGMENT).
 OS Streptococcus gordoni.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-P4A7;
 RA Chatenay-Rivauday C., Yamodo I., Sciotti M.A., Troffer-Charlier N.,
 RA Klein J.P., Ogier J.;
 RT "TNFalpha release by monocytic THP-1 cells through cross-linking of
 RT the extended V-region of the oral streptococcal protein I/II.";
 RL J. Leukoc. Biol. 0:0-0(2000).
 DR EMBL: AF192472; AAF20187.1; -.
 FT NON_TER 1
 FT 388 388

SEQ SEQUENCE 388 AA; 42720 MW; 907F6A76805BCE45 CRC64;

Query Match 9.7%; Score 78; DB 2; Length 388;

Best Local Similarity 20.1%; Pred. No. 14; Matches 27; Conservative 25; Mismatches 70; Indels 12; Gaps 3;

QY 28 VEDPDITDIDQASSEPOTRLIIMYKDESEVRGLAVTLVSKDSKSTLSCNKKIISFEEMDPEN 87
 DB 169 YKRYIVDSSQFKPNKNGVWLGIFDPLIGVAFASATYQGVKQDLSLFIKNEFTFYDENDQ 228
 QY 88 PENIDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKED-----DAFKLIKKK 139
 DB 229 PINFDNALLSVASLNR-----HNSIEMAKD-YSGTFIKISSGISEKNGMAYATFKTLNPRK 284
 QY 140 DENGKDSVMTITLN 153
 DB 285 DQGSRRMTYPRAN 298

RESULT 14

ID Q45916 PRELIMINARY; PRT; 1196 AA.

AC Q45916;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DE 01-JUN-2000 (Tremblrel. 14, Last annotation update)
 DE 138 KDA PROTEIN ASSOCIATED WITH BONT /CI-HAEMAGGLUTININ COMPLEX.
 GN CHN-138.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 CC Clostridium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hauser D.F., Eklund M.W., Popoff M.R.;
 RL Submitted (MAY-1992) to the EMBL/Genbank/DBJ databases.
 DR EMBL: X66433; CAA47059.1; -.
 DR INTERPRO: IPR000395; -.
 DR PFAM: PF01742; Peptidase_M27; 1.
 DR PRINTS: PRO0760; BONTOKIIXSIN.
 DR PRODOM: PD001963; -; 1.
 SQ SEQUENCE 1196 AA; 138725 MW; 88D5956301FA4A91 CRC64;

Query Match 9.7%; Score 78; DB 2; Length 1196;

Best Local Similarity 24.3%; Pred. No. 53; Matches 35; Conservative 23; Mismatches 58; Indels 28; Gaps 4;

QY 35 IDQASSEPOTRLIIMYKDESEVRGLAV--TLVSKDSKSTLSCNKKIISFEEMDPEN-- 90
 DB 965 ISISVDRKQDLIFIT-NDKNVANVSIDQILSIYTNISLVNKNNSIYVELSVLDNPI 1023
 QY 91 -----IDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDDAFK 133
 DB 1024 TSEEVIRNYSYLDNSYIRDSKSLLEYKNKYQLYNYVFPETSLYE-----VNDNKNKY 1077
 QY 134 LILKKKDENGKDSVMTITLNHOS 157
 DB 1078 LSLKNTDGINISSVKFKLINIDES 1101

RESULT 15

ID Q53550 PRELIMINARY; PRT; 1196 AA.

AC Q53550;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DE 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE PROGENITOR TOXIN T. NONTOKIC-NONHEMAGGLUTININ COMPONENT (FRAGMENT).
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 CC Clostridium.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 96025415.
 RA Ohyama T., Watanabe T., Fujinaga Y., Inoue K., Sunagawa H., Fujii N.,
 RA Inoue K., Ogura K.;
 RT "Characterization of nontoxic-nonhemagglutinin component of the two
 RT types of progenitor toxin (M and L) produced by Clostridium botulinum
 RT type D CB-16.";
 RL Microbiol. Immunol. 39:457-465(1995).
 DR EMBL: S80809; AAB36016.2; -.
 DR INTERPRO: IPR000395; -.
 DR PFAM: PF01742; Peptidase_M27; 1.
 FT NON_TER
 SQ SEQUENCE 1196 AA; 138717 MW; 6D2DBB5F6AF38324 CRC64;

Query Match 9.7%; Score 78; DB 2; Length 1196;

Best Local Similarity 24.3%; Pred. No. 53; Matches 35; Conservative 23; Mismatches 58; Indels 28; Gaps 4;

QY 35 IDQASSEPOTRLIIMYKDESEVRGLAV--TLVSKDSKSTLSCNKKIISFEEMDPEN-- 90
 DB 965 ISISVDRKQDLIFIT-NDKNVANVSIDQILSIYTNISLVNKNNSIYVELSVLDNPI 1023
 QY 91 -----IDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDDAFK 133
 DB 1024 TSEEVIRNYSYLDNSYIRDSKSLLEYKNKYQLYNYVFPETSLYE-----VNDNKNKY 1077
 QY 134 LILKKKDENGKDSVMTITLNHOS 157
 DB 1078 LSLKNTDGINISSVKFKLINIDES 1101

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